



#4

1

## SEQUENCE LISTING

<110> GEORGE, LISLE W  
ANGELOS, JOHN A  
HESS, JOHN F

<120> MORAXELLA BOVIS CYTOTOXIN, CYTOTOXIN GENE, ANTIBODIES  
AND VACCINES FOR PREVENTION AND TREATMENT OF MORAXELLA  
BOVIS INFECTIONS

<130> 481.06

<140> 09/884,696  
<141> 2001-06-19

<160> 41

<170> PatentIn Ver. 2.1

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Asp Arg Val Phe Tyr Ser Lys Asp Gly Gly Phe Gly Asn Ile Thr Val	
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Lys Leu Ser Ala Ser Asp Ile Ala Ser Ser Leu Asn Lys Leu Val Gly	
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Ser Met Ala Leu Phe Gly Thr Ala Asn Ser Val Ser Asn Ala Leu	
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Asp Glu Leu Gly Ile Ala Arg Leu Ala Glu Glu Pro Asn His Thr Glu	
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 645 650 655  
 Lys Val Gly Lys Arg Thr Glu Thr Ile Gln Tyr Arg Asp Tyr Glu Leu  
 660 665 670  
 Arg Lys Val Gly Tyr Gly Tyr Gln Ser Thr Asp Asn Leu Lys Ser Val  
 675 680 685

Glu Glu Val Ile Gly Ser Gln Phe Asn Asp Val Phe Lys Gly Ser Lys  
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Arg Asn Asn Ile Ala Thr Ala Gln Thr Ser Leu Gly Thr Ile Gln Thr  
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Ala Ile Gly Leu Thr Glu Arg Gly Ile Val Leu Ser Ala Pro Gln Ile  
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Asp Lys Leu Leu Gln Lys Thr Lys Ala Gly Gln Ala Leu Gly Ser Ala  
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Glu Ser Ile Val Gln Asn Ala Asn Lys Ala Lys Thr Val Leu Ser Gly  
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Ile Gln Ser Ile Leu Gly Ser Val Leu Ala Gly Met Asp Leu Asp Glu  
 145 150 155 160

Ala Leu Gln Asn Asn Ser Asn Gln His Ala Leu Ala Lys Ala Gly Leu  
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Ala Lys Lys Val Gly Ala Gly Phe Glu Leu Ala Asn Gln Val Val Gly  
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Asn Ile Thr Lys Ala Val Ser Ser Tyr Ile Leu Ala Gln Arg Val Ala  
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Ala Gly Leu Ser Ser Thr Gly Pro Val Ala Ala Leu Ile Ala Ser Thr  
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 His Asn Lys Ile Val Glu Trp Glu Lys Asn Asn His Gly Lys Asn Tyr  
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 Lys Thr Gln His Ile Leu Phe Arg Thr Pro Leu Leu Thr Pro Gly Thr  
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 Glu His Arg Glu Arg Val Gln Thr Gly Lys Tyr Glu Tyr Ile Thr Lys  
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Gly Ser Tyr Thr Val Asn Arg Phe Val Glu Thr Gly Lys Ala Leu His  
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Ile Glu Tyr Arg His Ser Asn Asn Gln His His Ala Gly Tyr Tyr Thr  
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Lys Asp Thr Leu Lys Ala Val Glu Glu Ile Ile Gly Thr Ser His Asn  
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Gly Lys Gly Asp Asp Ile Leu Asp Gly Gly Asn Gly Asp Asp Phe Ile  
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Glu Val Pro Asn Tyr Lys Ala Thr Lys Asp Glu Lys Ile Glu Glu Ile  
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 Ile Ser Gly Leu Leu Ser Gly Ala Ser Ala Gly Leu Ile Leu Ala Asp  
 245 250 255

Lys Glu Ala Ser Thr Glu Lys Ala Ala Ala Gly Val Glu Phe Ala  
 260 265 270  
 Asn Gln Ile Ile Gly Asn Val Thr Lys Ala Val Ser Ser Tyr Ile Leu  
 275 280 285  
 Ala Gln Arg Val Ala Ser Gly Leu Ser Ser Thr Gly Pro Val Ala Ala  
 290 295 300  
 Leu Ile Ala Ser Thr Val Ala Leu Ala Val Ser Pro Leu Ser Phe Leu  
 305 310 315 320  
 Asn Val Ala Asp Lys Phe Lys Gln Ala Asp Leu Ile Lys Ser Tyr Ser  
 325 330 335  
 Glu Arg Phe Gln Lys Leu Gly Tyr Asp Gly Asp Arg Leu Leu Ala Asp  
 340 345 350  
 Phe His Arg Glu Thr Gly Thr Ile Asp Ala Ser Val Thr Thr Ile Asn  
 355 360 365  
 Thr Ala Leu Ala Ala Ile Ser Gly Gly Val Gly Ala Ala Ser Ala Gly  
 370 375 380  
 Ser Leu Val Gly Ala Pro Val Ala Leu Leu Val Ala Gly Val Thr Gly  
 385 390 395 400  
 Leu Ile Thr Thr Ile Leu Glu Tyr Ser Lys Gln Ala Met Phe Glu His  
 405 410 415  
 Val Ala Asn Lys Val His Asp Arg Ile Val Glu Trp Glu Lys Lys His  
 420 425 430  
 Asn Lys Asn Tyr Phe Glu Gln Gly Tyr Asp Ser Arg His Leu Ala Asp  
 435 440 445  
 Leu Gln Asp Asn Met Lys Phe Leu Ile Asn Leu Asn Lys Glu Leu Gln  
 450 455 460  
 Ala Glu Arg Val Val Ala Ile Thr Gln Gln Arg Trp Asp Asn Gln Ile  
 465 470 475 480  
 Gly Asp Leu Ala Ala Ile Ser Arg Arg Thr Asp Lys Ile Ser Ser Gly  
 485 490 495  
 Lys Ala Tyr Val Asp Ala Phe Glu Glu Gly Gln His Gln Ser Tyr Asp  
 500 505 510  
 Ser Ser Val Gln Leu Asp Asn Lys Asn Gly Ile Ile Asn Ile Ser Asn  
 515 520 525  
 Thr Asn Arg Lys Thr Gln Ser Val Leu Phe Arg Thr Pro Leu Leu Thr  
 530 535 540  
 Pro Gly Glu Glu Asn Arg Glu Arg Ile Gln Glu Gly Lys Asn Ser Tyr  
 545 550 555 560

Ile Thr Lys Leu His Ile Gln Arg Val Asp Ser Trp Thr Val Thr Asp  
 565 570 575  
 Gly Asp Ala Ser Ser Ser Val Asp Phe Thr Asn Val Val Gln Arg Ile  
 580 585 590  
 Ala Val Lys Phe Asp Asp Ala Gly Asn Ile Ile Glu Ser Lys Asp Thr  
 595 600 605  
 Lys Ile Ile Ala Asn Leu Gly Ala Gly Asn Asp Asn Val Phe Val Gly  
 610 615 620  
 Ser Ser Thr Thr Val Ile Asp Gly Gly Asp Gly His Asp Arg Val His  
 625 630 635 640  
 Tyr Ser Arg Gly Glu Tyr Gly Ala Leu Val Ile Asp Ala Thr Ala Glu  
 645 650 655  
 Thr Glu Lys Gly Ser Tyr Ser Val Lys Arg Tyr Val Gly Asp Ser Lys  
 660 665 670  
 Ala Leu His Glu Thr Ile Ala Thr His Gln Thr Asn Val Gly Asn Arg  
 675 680 685  
 Glu Glu Lys Ile Glu Tyr Arg Arg Glu Asp Asp Arg Phe His Thr Gly  
 690 695 700  
 Tyr Thr Val Thr Asp Ser Leu Lys Ser Val Glu Glu Ile Ile Gly Ser  
 705 710 715 720  
 Gln Phe Asn Asp Ile Phe Lys Gly Ser Gln Phe Asp Asp Val Phe His  
 725 730 735  
 Gly Gly Asn Gly Val Asp Thr Ile Asp Gly Asn Asp Gly Asp Asp His  
 740 745 750  
 Leu Phe Gly Gly Ala Gly Asp Asp Val Ile Asp Gly Gly Asn Gly Asn  
 755 760 765  
 Asn Phe Leu Val Gly Gly Thr Gly Asn Asp Ile Ile Ser Gly Gly Lys  
 770 775 780  
 Asp Asn Asp Ile Tyr Val His Lys Thr Gly Asp Gly Asn Asp Ser Ile  
 785 790 795 800  
 Thr Asp Ser Gly Gly Gln Asp Lys Leu Ala Phe Ser Asp Val Asn Leu  
 805 810 815  
 Lys Asp Leu Thr Phe Lys Lys Val Asp Ser Ser Leu Glu Ile Ile Asn  
 820 825 830  
 Gln Lys Gly Glu Lys Val Arg Ile Gly Asn Trp Phe Leu Glu Asp Asp  
 835 840 845  
 Leu Ala Ser Thr Val Ala Asn Tyr Lys Ala Thr Asn Asp Arg Lys Ile  
 850 855 860

Glu Glu Ile Ile Gly Lys Gly Gly Glu Arg Ile Thr Ser Glu Gln Val  
 865 870 875 880

Asp Lys Leu Ile Lys Glu Gly Asn Asn Gln Ile Ser Ala Glu Ala Leu  
 885 890 895

Ser Lys Val Val Asn Asp Tyr Asn Thr Ser Lys Asp Arg Gln Asn Val  
 900 905 910

Ser Asn Ser Leu Ala Lys Leu Ile Ser Ser Val Gly Ser Phe Thr Ser  
 915 920 925

Ser Ser Asp Phe Arg Asn Asn Leu Gly Thr Tyr Val Pro Ser Ser Ile  
 930 935 940

Asp Val Ser Asn Asn Ile Gln Leu Ala Arg Ala Ala  
 945 950 955

<210> 5  
 <211> 1023  
 <212> PRT  
 <213> Escherichia coli

<400> 5  
 Met Pro Thr Ile Thr Ala Ala Gln Ile Lys Ser Thr Leu Gln Ser Ala  
 1 5 10 15

Lys Gln Ser Ala Ala Asn Lys Leu His Ser Ala Gly Gln Ser Thr Lys  
 20 25 30

Asp Ala Leu Lys Lys Ala Ala Glu Gln Thr Arg Asn Ala Gly Asn Arg  
 35 40 45

Leu Ile Leu Leu Ile Pro Lys Asp Tyr Lys Gly Gln Gly Ser Ser Leu  
 50 55 60

Asn Asp Leu Val Arg Thr Ala Asp Glu Leu Gly Ile Glu Val Gln Tyr  
 65 70 75 80

Asp Glu Lys Asn Gly Thr Ala Ile Thr Lys Gln Val Phe Gly Thr Ala  
 85 90 95

Glu Lys Leu Ile Gly Leu Thr Glu Arg Gly Val Thr Ile Phe Ala Pro  
 100 105 110

Gln Leu Asp Lys Leu Leu Gln Lys Tyr Gln Lys Ala Gly Asn Lys Leu  
 115 120 125

Gly Gly Ser Ala Glu Asn Ile Gly Asp Asn Leu Gly Lys Ala Gly Ser  
 130 135 140

Val Leu Ser Thr Phe Gln Asn Phe Leu Gly Thr Ala Leu Ser Ser Met  
 145 150 155 160

Lys Ile Asp Glu Leu Ile Lys Lys Gln Lys Ser Gly Gly Asn Val Ser  
 165 170 175

Ser Ser Glu Leu Ala Lys Ala Ser Ile Glu Leu Ile Asn Gln Leu Val  
 180 185 190  
 Asp Thr Ala Ala Ser Leu Asn Asn Val Asn Ser Phe Ser Gln Gln Leu  
 195 200 205  
 Asn Lys Leu Gly Ser Val Leu Ser Asn Thr Lys His Leu Asn Gly Val  
 210 215 220  
 Gly Asn Lys Leu Gln Asn Leu Pro Asn Leu Asp Asn Ile Gly Ala Gly  
 225 230 235 240  
 Leu Asp Thr Val Ser Gly Ile Leu Ser Ala Ile Ser Ala Ser Phe Ile  
 245 250 255  
 Leu Ser Asn Ala Asp Ala Asp Thr Gly Thr Lys Ala Ala Ala Gly Val  
 260 265 270  
 Glu Leu Thr Thr Lys Val Leu Gly Asn Val Gly Lys Gly Ile Ser Gln  
 275 280 285  
 Tyr Ile Ile Ala Gln Arg Ala Ala Gln Gly Leu Ser Thr Ser Ala Ala  
 290 295 300  
 Ala Ala Gly Leu Ile Ala Ser Val Val Thr Leu Ala Ile Ser Pro Leu  
 305 310 315 320  
 Ser Phe Leu Ser Ile Ala Asp Lys Phe Lys Arg Ala Asn Lys Ile Glu  
 325 330 335  
 Glu Tyr Ser Gln Arg Phe Lys Lys Leu Gly Tyr Asp Gly Asp Ser Leu  
 340 345 350  
 Leu Ala Ala Phe His Lys Glu Thr Gly Ala Ile Asp Ala Ser Leu Thr  
 355 360 365  
 Arg Ile Ser Thr Val Leu Ala Ser Val Ser Ser Gly Ile Ser Ala Ala  
 370 375 380  
 Ala Thr Thr Ser Leu Val Gly Ala Pro Val Ser Ala Leu Val Gly Ala  
 385 390 395 400  
 Val Thr Gly Ile Ile Ser Gly Ile Leu Glu Ala Ser Lys Gln Ala Met  
 405 410 415  
 Phe Glu His Val Ala Ser Lys Met Ala Asp Val Ile Ala Glu Trp Glu  
 420 425 430  
 Lys Lys His Gly Lys Asn Tyr Phe Glu Asn Gly Tyr Asp Ala Arg His  
 435 440 445  
 Ala Ala Phe Leu Glu Asp Asn Phe Lys Ile Leu Ser Gln Tyr Asn Lys  
 450 455 460  
 Glu Tyr Ser Val Glu Arg Ser Val Leu Ile Thr Gln Gln His Trp Asp  
 465 470 475 480

Thr Leu Ile Gly Glu Leu Ala Gly Val Thr Arg Asn Gly Asp Lys Thr  
 485 490 495

Leu Ser Gly Lys Ser Tyr Ile Asp Tyr Tyr Glu Glu Gly Lys Arg Leu  
 500 505 510

Glu Lys Lys Pro Asp Glu Phe Gln Lys Gln Val Phe Asp Pro Leu Lys  
 515 520 525

Gly Asn Ile Asp Leu Ser Asp Ser Lys Ser Ser Thr Leu Leu Lys Phe  
 530 535 540

Val Thr Pro Leu Leu Thr Pro Gly Glu Glu Ile Arg Glu Arg Arg Gln  
 545 550 555 560

Ser Gly Lys Tyr Glu Tyr Ile Thr Glu Leu Leu Val Lys Gly Val Asp  
 565 570 575

Lys Trp Thr Val Lys Gly Val Gln Asp Lys Gly Ser Val Tyr Asp Tyr  
 580 585 590

Ser Asn Leu Ile Gln His Ala Ser Val Gly Asn Asn Gln Tyr Arg Glu  
 595 600 605

Ile Arg Ile Glu Ser His Leu Gly Asp Gly Asp Asp Lys Val Phe Leu  
 610 615 620

Ser Ala Gly Ser Ala Asn Ile Tyr Ala Gly Lys Gly His Asp Val Val  
 625 630 635 640

Tyr Tyr Asp Lys Thr Asp Thr Gly Tyr Leu Thr Ile Asp Gly Thr Lys  
 645 650 655

Ala Thr Glu Ala Gly Asn Tyr Thr Val Thr Arg Val Leu Gly Gly Asp  
 660 665 670

Val Lys Val Leu Gln Glu Val Val Lys Glu Gln Glu Val Ser Val Gly  
 675 680 685

Lys Arg Thr Glu Lys Thr Gln Tyr Arg Ser Tyr Glu Phe Thr His Ile  
 690 695 700

Asn Gly Lys Asn Leu Thr Glu Thr Asp Asn Leu Tyr Ser Val Glu Glu  
 705 710 715 720

Leu Ile Gly Thr Thr Arg Ala Asp Lys Phe Phe Gly Ser Lys Phe Ala  
 725 730 735

Asp Ile Phe His Gly Ala Asp Gly Asp Asp His Ile Glu Gly Asn Asp  
 740 745 750

Gly Asn Asp Arg Leu Tyr Gly Asp Lys Gly Asn Asp Thr Leu Ser Gly  
 755 760 765

Gly Asn Gly Asp Asp Gln Leu Tyr Gly Asp Gly Asn Asp Lys Leu  
 770 775 780

Ile Gly Gly Ala Gly Asn Asn Tyr Leu Asn Gly Gly Asp Gly Asp Asp  
 785 790 795 800

Glu Leu Gln Val Gln Gly Asn Ser Leu Ala Lys Asn Val Leu Ser Gly  
 805 810 815

Gly Lys Gly Asn Asp Lys Leu Tyr Gly Ser Glu Gly Ala Asp Leu Leu  
 820 825 830

Asp Gly Gly Glu Gly Asn Asp Leu Leu Lys Gly Gly Tyr Gly Asn Asp  
 835 840 845

Ile Tyr Arg Tyr Leu Ser Gly Tyr Gly His His Ile Ile Asp Asp Asp  
 850 855 860

Gly Gly Lys Asp Asp Lys Leu Ser Leu Ala Asp Ile Asp Phe Arg Asp  
 865 870 875 880

Val Ala Phe Arg Arg Glu Gly Asn Asp Leu Ile Met Tyr Lys Ala Glu  
 885 890 895

Gly Asn Val Leu Ser Ile Gly His Lys Asn Gly Ile Thr Phe Lys Asn  
 900 905 910

Trp Phe Glu Lys Glu Ser Gly Asp Ile Ser Asn His Gln Ile Glu Gln  
 915 920 925

Ile Phe Asp Lys Asp Gly Arg Val Ile Thr Pro Asp Ser Leu Lys Lys  
 930 935 940

Ala Leu Glu Tyr Gln Gln Ser Asn Asn Lys Ala Ser Tyr Val Tyr Gly  
 945 950 955 960

Asn Asp Ala Leu Ala Tyr Gly Ser Gln Gly Asn Leu Asn Pro Leu Ile  
 965 970 975

Asn Glu Ile Ser Lys Ile Ile Ser Ala Ala Gly Asn Phe Asp Val Lys  
 980 985 990

Glu Glu Arg Ala Ala Ser Leu Leu Gln Leu Ser Gly Asn Ala Ser  
 995 1000 1005

Asp Phe Ser Tyr Gly Arg Asn Ser Ile Thr Leu Thr Ala Ser Ala  
 1010 1015 1020

<210> 6  
 <211> 12  
 <212> PRT  
 <213> *Moraxella bovis*

<400> 6  
 Phe Leu Ser Glu Leu Asn Lys Glu Leu Glu Ala Glu  
 1 5 10

<210> 7  
 <211> 12

<212> PRT

<213> Pasteurella haemolytica

<400> 7

Phe Leu Leu Asn Leu Asn Lys Glu Leu Gln Ala Glu  
1 5 10

<210> 8

<211> 12

<212> PRT

<213> Escherichia coli

<400> 8

Ile Leu Ser Gln Tyr Asn Lys Glu Tyr Ser Val Glu  
1 5 10

<210> 9

<211> 12

<212> PRT

<213> Actinobacillus pleuropneumoniae

<400> 9

Phe Leu Ile Asn Leu Asn Lys Glu Leu Gln Ala Glu  
1 5 10

<210> 10

<211> 12

<212> PRT

<213> Actinobacillus pleuropneumoniae

<400> 10

Leu Leu Ser Gln Tyr Asn Lys Glu Tyr Ser Val Glu  
1 5 10

<210> 11

<211> 12

<212> PRT

<213> Actinobacillus suis

<400> 11

Phe Leu Ile Asn Leu Asn Lys Glu Leu Gln Ala Glu  
1 5 10

<210> 12

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: consensus  
sequence

<220>  
<221> MOD\_RES  
<222> (3)  
<223> L, Y, A or V

<220>  
<221> MOD\_RES  
<222> (7)..(8)  
<223> L, Y, A or V

<400> 12  
Phe Leu Xaa Asn Lys Glu Xaa Xaa Glu  
1 5

<210> 13  
<211> 14  
<212> PRT  
<213> *Moraxella bovis*

<400> 13  
Phe Asn Asp Ile Phe His Ser Gly Glu Gly Asp Asp Leu Leu  
1 5 10

<210> 14  
<211> 14  
<212> PRT  
<213> *Actinobacillus pleuropneumoniae*

<400> 14  
Phe Arg Asp Ile Phe His Gly Ala Asp Gly Asp Asp Leu Leu  
1 5 10

<210> 15  
<211> 14  
<212> PRT  
<213> *Actinobacillus actinomycetemcomitans*

<400> 15  
Phe Asn Asp Val Phe His Gly His Asp Gly Asp Asp Leu Ile  
1 5 10

<210> 16  
<211> 14  
<212> PRT  
<213> *Actinobacillus pleuropneumoniae*

<400> 16  
Phe Arg Asp Ile Phe His Gly Ala Asp Gly Asp Asp Leu Leu  
1 5 10

<210> 17  
<211> 11

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: consensus  
sequence

&lt;220&gt;

&lt;221&gt; MOD\_RES

&lt;222&gt; (11)

&lt;223&gt; L or I

&lt;400&gt; 17

Phe Asp Phe His Gly Ala Asp Gly Asp Asp Xaa  
1 5 10

&lt;210&gt; 18

&lt;211&gt; 737

&lt;212&gt; PRT

&lt;213&gt; Moraxella bovis

&lt;400&gt; 18

Met Gly Gly Asp Thr Ser Leu Ile Arg Leu Asn Leu Gln Thr Leu Asn  
1 5 10 15Ser Asn Leu Val Met Ile Asp Tyr Ala Gln Gln Pro Ala Leu Ser Ala  
20 25 30Leu Val Ile Leu Ala Lys Tyr Tyr Gly Ile Ser Ala Ser Pro Ala Asp  
35 40 45Ile Met His Gln Phe Ser Asp Asn Thr Lys Gly Asp Leu Asn Glu Ile  
50 55 60Glu Trp Met Leu Ala Ala Lys Lys Leu Glu Leu Lys Val Lys Ile Ile  
65 70 75 80Lys Gln Pro Leu Thr Arg Leu Ser Met Ile Thr Leu Pro Ala Leu Val  
85 90 95Trp Cys Asp Asn Lys Pro Asp Leu Asp Gln Asn Leu Asn Ser His Phe  
100 105 110Ile Leu Thr Lys Ile Asp Gly Val Gly Ser Ala Ala Lys Tyr Leu Ile  
115 120 125Tyr Asp Leu Ile Glu Asn Arg Pro Ile Ile Leu Asp Ala Ser Glu Phe  
130 135 140Ser Glu Arg Tyr Ser Gly Lys Leu Met Leu Val Thr Ser Arg Ala Ser  
145 150 155 160Ile Leu Gly Ser Leu Ala Lys Phe Asp Phe Thr Trp Phe Ile Pro Ala  
165 170 175Val Ile Lys Tyr Arg Tyr Ile Phe Phe Glu Val Ile Val Ile Ser Val  
180 185 190

Val Leu Gln Ile Phe Ala Leu Ile Thr Pro Leu Phe Phe Gln Val Val  
 195 200 205

Met Asp Lys Val Leu Val His Arg Gly Phe Ser Thr Leu Asp Val Val  
 210 215 220

Ala Ile Ala Leu Leu Val Val Ser Leu Phe Glu Val Ile Leu Ser Gly  
 225 230 235 240

Leu Arg Thr Tyr Ile Phe Ala His Thr Thr Ser Arg Ile Asp Val Glu  
 245 250 255

Leu Gly Ala Arg Leu Phe Arg His Leu Leu Ala Leu Pro Leu Ala Tyr  
 260 265 270

Phe Glu Ser Arg Arg Val Gly Asp Thr Val Ala Arg Ile Arg Glu Leu  
 275 280 285

Glu His Ile Arg Asn Phe Leu Thr Gly Gln Ala Leu Thr Ser Val Leu  
 290 295 300

Asp Leu Val Phe Ser Phe Ile Phe Leu Phe Val Met Trp Tyr Tyr Ser  
 305 310 315 320

Pro Thr Leu Thr Leu Val Val Leu Ala Ser Leu Pro Ile Tyr Ala Phe  
 325 330 335

Trp Ser Ala Phe Ile Ser Pro Ile Leu Arg Thr Arg Leu Asn Asp Gln  
 340 345 350

Phe Ala Arg Asn Ala Asp Asn Gln Ser Phe Leu Val Glu Ser Ile Thr  
 355 360 365

Ala Val Gly Thr Val Lys Ala Met Ala Val Glu Pro Gln Met Thr Arg  
 370 375 380

Arg Trp Asp Asn Gln Leu Ala Ala Tyr Val Val Ser Ser Phe Arg Val  
 385 390 395 400

Ala Lys Leu Ala Met Val Gly Gln Gln Gly Val Gln Leu Ile Gln Lys  
 405 410 415

Met Val Ile Val Ala Thr Leu Trp Ile Gly Ala Lys Leu Val Ile Glu  
 420 425 430

Gly Lys Leu Ser Val Gly Gln Leu Ile Ala Phe Asn Met Leu Ala Gly  
 435 440 445

Gln Val Ala Ala Pro Val Ile Arg Leu Ala Gln Leu Trp Gln Asp Phe  
 450 455 460

Gln Gln Val Gly Ile Ser Val Ala Arg Leu Gly Asp Ile Leu Asn Thr  
 465 470 475 480

Pro Thr Glu His Ser Thr Ser Arg Leu Thr Leu Pro Asp Ile Lys Gly  
 485 490 495

Asp Ile Thr Phe Glu Asn Val Asp Phe Arg Tyr Lys Ile Asp Gly His  
 500 505 510  
 Leu Ile Leu Gln Asn Leu Asn Leu Gln Ile Asn Ala Gly Glu Ile Leu  
 515 520 525  
 Gly Ile Val Gly Arg Ser Gly Ser Gly Lys Ser Thr Leu Thr Lys Leu  
 530 535 540  
 Val Gln Arg Leu Tyr Val Pro Glu Asn Gly Arg Ile Leu Val Asp Gly  
 545 550 555 560  
 Asn Asp Leu Ala Leu Ala Asp Pro Ala Trp Leu Arg Arg Gln Val Gly  
 565 570 575  
 Val Val Leu Gln Glu Asn Val Leu Leu Asn Arg Ser Ile Arg Asp Asn  
 580 585 590  
 Ile Ala Leu Thr Asp Thr Gly Met Ser Leu Glu Phe Ile Ile Gln Ala  
 595 600 605  
 Ala Lys Met Ser Gly Ala His Asp Phe Ile Met Glu Leu Pro Glu Gly  
 610 615 620  
 Tyr Asp Thr Ile Val Gly Glu Gln Gly Ala Gly Leu Ser Gly Gly Gln  
 625 630 635 640  
 Arg Gln Arg Ile Ala Ile Ala Arg Ala Leu Ile Thr Asn Pro Arg Ile  
 645 650 655  
 Leu Ile Phe Asp Glu Ala Thr Ser Ala Leu Asp Tyr Glu Ser Glu Arg  
 660 665 670  
 Ala Ile Met Gln Asn Met Gln Ala Ile Cys Gln Gly Arg Thr Val Leu  
 675 680 685  
 Ile Ile Ala His Arg Leu Ser Thr Val Lys Met Ala His Arg Ile Ile  
 690 695 700  
 Ala Met Asp Lys Gly Lys Ile Val Glu Gln Gly Thr His Gln Glu Leu  
 705 710 715 720  
 Leu Gln Lys Glu Asp Gly Tyr Tyr Arg Tyr Leu Tyr Asp Leu Gln Asn  
 725 730 735  
 Gly

<210> 19  
 <211> 708  
 <212> PRT  
 <213> *Pasteurella haemolytica*  
 <400> 19  
 Met Glu Ala Asn His Gln Arg Asn Asp Leu Gly Leu Val Ala Leu Thr  
 1 5 10 15

Met Leu Ala Gln Tyr His Asn Ile Ser Leu Asn Pro Glu Glu Ile Lys  
 20 25 30

His Lys Phe Asp Leu Asp Gly Lys Gly Leu Ser Leu Thr Ala Trp Leu  
 35 40 45

Leu Ala Ala Lys Ser Leu Ala Leu Lys Ala Lys His Ile Lys Lys Glu  
 50 55 60

Ile Ser Arg Leu His Leu Val Asn Leu Pro Ala Leu Val Trp Gln Asp  
 65 70 75 80

Asn Gly Lys His Phe Leu Leu Val Lys Val Asp Thr Asp Asn Asn Arg  
 85 90 95

Tyr Leu Thr Tyr Asn Leu Glu Gln Asp Ala Pro Gln Ile Leu Ser Thr  
 100 105 110

Asp Glu Phe Glu Ala Cys Tyr Gln Gly Gln Leu Ile Leu Val Thr Ser  
 115 120 125

Arg Ala Ser Val Val Gly Gln Leu Ala Lys Phe Asp Phe Thr Trp Phe  
 130 135 140

Ile Pro Ala Val Ile Lys Tyr Arg Lys Ile Phe Leu Glu Thr Leu Ile  
 145 150 155 160

Val Ser Ile Phe Leu Gln Ile Phe Ala Leu Ile Thr Pro Leu Phe Phe  
 165 170 175

Gln Val Val Met Asp Lys Val Leu Val His Arg Gly Phe Ser Thr Leu  
 180 185 190

Asn Ile Ile Thr Val Ala Leu Ala Ile Val Ile Ile Phe Glu Ile Val  
 195 200 205

Leu Ser Gly Leu Arg Thr Tyr Val Phe Ser His Ser Thr Ser Arg Ile  
 210 215 220

Asp Val Glu Leu Gly Ala Lys Leu Phe Arg His Leu Leu Ser Leu Pro  
 225 230 235 240

Ile Ser Tyr Phe Glu Asn Arg Arg Val Gly Asp Thr Val Ala Arg Val  
 245 250 255

Arg Glu Leu Asp Gln Ile Arg Asn Phe Leu Thr Gly Gln Ala Leu Thr  
 260 265 270

Ser Val Leu Asp Leu Leu Phe Ser Phe Ile Phe Phe Ala Val Met Trp  
 275 280 285

Tyr Tyr Ser Pro Lys Leu Thr Leu Val Ile Leu Gly Ser Leu Pro Cys  
 290 295 300

Tyr Ile Leu Trp Ser Ile Phe Ile Ser Pro Ile Leu Arg Arg Arg Leu  
 305 310 315 320

Asp Glu Lys Phe Ala Arg Ser Ala Asp Asn Gln Ala Phe Leu Val Glu  
 325 330 335

Ser Val Thr Ala Ile Asn Met Ile Lys Ala Met Ala Val Ala Pro Gln  
 340 345 350

Met Thr Asp Thr Trp Asp Lys Gln Leu Ala Ser Tyr Val Ser Ser Ser  
 355 360 365

Phe Arg Val Thr Val Leu Ala Thr Ile Gly Gln Gln Gly Val Gln Leu  
 370 375 380

Ile Gln Lys Thr Val Met Val Ile Asn Leu Trp Leu Gly Ala His Leu  
 385 390 395 400

Val Ile Ser Gly Asp Leu Ser Ile Gly Gln Leu Ile Ala Phe Asn Met  
 405 410 415

Leu Ser Gly Gln Val Ile Ala Pro Val Ile Arg Leu Ala Gln Leu Trp  
 420 425 430

Gln Asp Phe Gln Gln Val Gly Ile Ser Val Thr Arg Leu Gly Asp Val  
 435 440 445

Leu Asn Ser Pro Thr Glu Gln Tyr Gln Gly Lys Leu Ser Leu Pro Glu  
 450 455 460

Ile Lys Gly Asp Ile Ser Phe Lys Asn Ile Arg Phe Arg Tyr Lys Pro  
 465 470 475 480

Asp Ala Pro Thr Ile Leu Asn Asn Val Asn Leu Glu Ile Arg Gln Gly  
 485 490 495

Glu Val Ile Gly Ile Val Gly Arg Ser Gly Ser Gly Lys Ser Thr Leu  
 500 505 510

Thr Lys Leu Leu Gln Arg Phe Tyr Ile Pro Glu Asn Gly Gln Val Leu  
 515 520 525

Ile Asp Gly His Asp Leu Ala Leu Ala Asp Pro Asn Trp Leu Arg Arg  
 530 535 540

Gln Ile Gly Val Val Leu Gln Asp Asn Val Leu Leu Asn Arg Ser Ile  
 545 550 555 560

Arg Glu Asn Ile Ala Leu Ser Asp Pro Gly Met Pro Met Glu Arg Val  
 565 570 575

Ile Tyr Ala Ala Lys Leu Ala Gly Ala His Asp Phe Ile Ser Glu Leu  
 580 585 590

Arg Glu Gly Tyr Asn Thr Ile Val Gly Glu Gln Gly Ala Gly Leu Ser  
 595 600 605

Gly Gly Gln Arg Gln Arg Ile Ala Ile Ala Arg Ala Leu Val Asn Asn  
 610 615 620

Pro Lys Ile Leu Ile Phe Asp Glu Ala Thr Ser Ala Leu Asp Tyr Glu  
 625 630 635 640

Ser Glu His Ile Ile Met Gln Asn Met Gln Lys Ile Cys Gln Gly Arg  
 645 650 655

Thr Val Ile Leu Ile Ala His Arg Leu Ser Thr Val Lys Asn Ala Asp  
 660 665 670

Arg Ile Ile Val Met Glu Lys Gly Glu Ile Val Glu Gln Gly Lys His  
 675 680 685

His Glu Leu Leu Gln Asn Ser Asn Gly Leu Tyr Ser Tyr Leu His Gln  
 690 695 700

Leu Gln Leu Asn  
 705

<210> 20

<211> 707

<212> PRT

<213> *Actinobacillus pleuropneumoniae*

<400> 20

Met Asp Phe Tyr Arg Glu Glu Asp Tyr Gly Leu Tyr Ala Leu Thr Ile  
 1 5 10 15

Leu Ala Gln Tyr His Asn Ile Ala Val Asn Pro Glu Glu Leu Lys His  
 20 25 30

Lys Phe Asp Leu Glu Gly Lys Gly Leu Asp Leu Thr Ala Trp Leu Leu  
 35 40 45

Ala Ala Lys Ser Leu Glu Leu Lys Ala Lys Gln Val Lys Lys Ala Ile  
 50 55 60

Asp Arg Leu Ala Phe Ile Ala Leu Pro Ala Leu Val Trp Arg Glu Asp  
 65 70 75 80

Gly Lys His Phe Ile Leu Thr Lys Ile Asp Asn Glu Ala Lys Lys Tyr  
 85 90 95

Leu Ile Phe Asp Leu Glu Thr His Asn Pro Arg Ile Leu Glu Gln Ala  
 100 105 110

Glu Phe Glu Ser Leu Tyr Gln Gly Lys Leu Ile Leu Val Ala Ser Arg  
 115 120 125

Ala Ser Ile Val Gly Lys Leu Ala Lys Phe Asp Phe Thr Trp Phe Ile  
 130 135 140

Pro Ala Val Ile Lys Tyr Arg Lys Ile Phe Ile Glu Thr Leu Ile Val  
 145 150 155 160

Ser Ile Phe Leu Gln Ile Phe Ala Leu Ile Thr Pro Leu Phe Phe Gln  
 165 170 175

Val Val Met Asp Lys Val Leu Val His Arg Gly Phe Ser Thr Leu Asn  
 180 185 190  
 Val Ile Thr Val Ala Leu Ala Ile Val Val Leu Phe Glu Ile Val Leu  
 195 200 205  
 Asn Gly Leu Arg Thr Tyr Ile Phe Ala His Ser Thr Ser Arg Ile Asp  
 210 215 220  
 Val Glu Leu Gly Ala Arg Leu Phe Arg His Leu Leu Ala Leu Pro Ile  
 225 230 235 240  
 Ser Tyr Phe Glu Asn Arg Arg Val Gly Asp Thr Val Ala Arg Val Arg  
 245 250 255  
 Glu Leu Asp Gln Ile Arg Asn Phe Leu Thr Gly Gln Ala Leu Thr Ser  
 260 265 270  
 Val Leu Asp Leu Met Phe Ser Phe Ile Phe Phe Ala Val Met Trp Tyr  
 275 280 285  
 Tyr Ser Pro Lys Leu Thr Leu Val Ile Leu Gly Ser Leu Pro Phe Tyr  
 290 295 300  
 Met Gly Trp Ser Ile Phe Ile Ser Pro Ile Leu Arg Arg Arg Leu Asp  
 305 310 315 320  
 Glu Lys Phe Ala Arg Gly Ala Asp Asn Gln Ser Phe Leu Val Glu Ser  
 325 330 335  
 Val Thr Ala Ile Asn Thr Ile Lys Ala Leu Ala Val Thr Pro Gln Met  
 340 345 350  
 Thr Asn Thr Trp Asp Lys Gln Leu Ala Ser Tyr Val Ser Ala Gly Phe  
 355 360 365  
 Arg Val Thr Thr Leu Ala Thr Ile Gly Gln Gln Gly Val Gln Phe Ile  
 370 375 380  
 Gln Lys Val Val Met Val Ile Thr Leu Trp Leu Gly Ala His Leu Val  
 385 390 395 400  
 Ile Ser Gly Asp Leu Ser Ile Gly Gln Leu Ile Ala Phe Asn Met Leu  
 405 410 415  
 Ser Gly Gln Val Ile Ala Pro Val Ile Arg Leu Ala Gln Leu Trp Gln  
 420 425 430  
 Asp Phe Gln Gln Val Gly Ile Ser Val Thr Arg Leu Gly Asp Val Leu  
 435 440 445  
 Asn Ser Pro Thr Glu Ser Tyr Gln Gly Lys Leu Ala Leu Pro Glu Ile  
 450 455 460  
 Lys Gly Asp Ile Thr Phe Arg Asn Ile Arg Phe Arg Tyr Lys Pro Asp  
 465 470 475 480

Ala Pro Val Ile Leu Asn Asp Val Asn Leu Ser Ile Gln Gln Gly Glu  
 485 490 495

Val Ile Gly Ile Val Gly Arg Ser Gly Ser Gly Lys Ser Thr Leu Thr  
 500 505 510

Lys Leu Ile Gln Arg Phe Tyr Ile Pro Glu Asn Gly Gln Val Leu Ile  
 515 520 525

Asp Gly His Asp Leu Ala Leu Ala Asp Pro Asn Trp Leu Arg Arg Gln  
 530 535 540

Val Gly Val Val Leu Gln Asp Asn Val Leu Leu Asn Arg Ser Ile Arg  
 545 550 555 560

Asp Asn Ile Ala Leu Ala Asp Pro Gly Met Pro Met Glu Lys Ile Val  
 565 570 575

His Ala Ala Lys Leu Ala Gly Ala His Glu Phe Ile Ser Glu Leu Arg  
 580 585 590

Glu Gly Tyr Asn Thr Ile Val Gly Glu Gln Gly Ala Gly Leu Ser Gly  
 595 600 605

Gly Gln Arg Gln Arg Ile Ala Ile Ala Arg Ala Leu Val Asn Asn Pro  
 610 615 620

Lys Ile Leu Ile Phe Asp Glu Ala Thr Ser Ala Leu Asp Tyr Glu Ser  
 625 630 635 640

Glu His Ile Ile Met Arg Asn Met His Gln Ile Cys Lys Gly Arg Thr  
 645 650 655

Val Ile Ile Ile Ala His Arg Leu Ser Thr Val Lys Asn Ala Asp Arg  
 660 665 670

Ile Ile Val Met Glu Lys Gly Gln Ile Val Glu Gln Gly Lys His Lys  
 675 680 685

Glu Leu Leu Ala Asp Pro Asn Gly Leu Tyr His Tyr Leu His Gln Leu  
 690 695 700

Gln Ser Glu  
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 <212> PRT  
 <213> Escherichia coli

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 20 25 30

Arg Phe Asp Thr Asp Gly Thr Gly Leu Gly Leu Thr Ser Trp Leu Leu  
 35 40 45

Ala Ala Lys Ser Leu Glu Leu Lys Val Lys Gln Val Lys Lys Thr Ile  
 50 55 60

Asp Arg Leu Asn Phe Ile Ser Leu Pro Ala Leu Val Trp Arg Glu Asp  
 65 70 75 80

Gly Arg His Phe Ile Leu Thr Lys Val Ser Lys Glu Ala Asn Arg Tyr  
 85 90 95

Leu Ile Phe Asp Leu Glu Gln Arg Asn Pro Arg Val Leu Glu Gln Ser  
 100 105 110

Glu Phe Glu Ala Leu Tyr Gln Gly His Ile Ile Leu Ile Ala Ser Arg  
 115 120 125

Ser Ser Val Ala Gly Lys Leu Ala Lys Phe Asp Phe Thr Trp Phe Ile  
 130 135 140

Pro Ala Ile Ile Lys Tyr Arg Arg Ile Phe Ile Glu Thr Leu Val Val  
 145 150 155 160

Ser Val Phe Leu Gln Leu Phe Ala Leu Ile Thr Pro Leu Phe Phe Gln  
 165 170 175

Val Val Met Asp Lys Val Leu Val His Arg Gly Phe Ser Thr Leu Asn  
 180 185 190

Val Ile Thr Val Ala Leu Ser Val Val Val Val Phe Glu Ile Ile Leu  
 195 200 205

Ser Gly Leu Arg Thr Tyr Ile Phe Ala His Ser Thr Ser Arg Ile Asp  
 210 215 220

Val Glu Leu Gly Ala Lys Leu Phe Arg His Leu Leu Ala Leu Pro Ile  
 225 230 235 240

Ser Tyr Phe Glu Ser Arg Arg Val Gly Asp Thr Val Ala Arg Val Arg  
 245 250 255

Glu Leu Asp Gln Ile Arg Asn Phe Leu Thr Gly Gln Ala Leu Thr Ser  
 260 265 270

Val Leu Asp Leu Leu Phe Ser Phe Ile Phe Phe Ala Val Met Trp Tyr  
 275 280 285

Tyr Ser Pro Lys Leu Thr Leu Val Ile Leu Phe Ser Leu Pro Cys Tyr  
 290 295 300

Ala Ala Trp Ser Val Phe Ile Ser Pro Ile Leu Arg Arg Arg Leu Asp  
 305 310 315 320

Asp Lys Phe Ser Arg Asn Ala Asp Asn Gln Ser Phe Leu Val Glu Ser  
 325 330 335

Val Thr Ala Ile Asn Thr Ile Lys Ala Met Ala Val Ser Pro Gln Met  
 340 345 350

Thr Asn Ile Trp Asp Lys Gln Leu Ala Gly Tyr Val Ala Ala Gly Phe  
 355 360 365

Lys Val Thr Val Leu Ala Thr Ile Gly Gln Gln Gly Ile Gln Leu Ile  
 370 375 380

Gln Lys Thr Val Met Ile Ile Asn Leu Trp Leu Gly Ala His Leu Val  
 385 390 395 400

Ile Ser Gly Asp Leu Ser Ile Gly Gln Leu Ile Ala Phe Asn Met Leu  
 405 410 415

Ala Gly Gln Ile Val Ala Pro Val Ile Arg Leu Ala Gln Ile Trp Gln  
 420 425 430

Asp Phe Gln Gln Val Gly Ile Ser Val Thr Arg Leu Gly Asp Val Leu  
 435 440 445

Asn Ser Pro Thr Glu Ser Tyr His Gly Lys Leu Ala Leu Pro Glu Ile  
 450 455 460

Asn Gly Asp Ile Thr Phe Arg Asn Ile Arg Phe Arg Tyr Lys Pro Asp  
 465 470 475 480

Ser Pro Val Ile Leu Asp Asn Ile Asn Leu Ser Ile Lys Gln Gly Glu  
 485 490 495

Val Ile Gly Ile Val Gly Arg Ser Gly Ser Gly Lys Ser Thr Leu Thr  
 500 505 510

Lys Leu Ile Gln Arg Phe Tyr Ile Pro Glu Asn Gly Gln Val Leu Ile  
 515 520 525

Asp Gly His Asp Leu Ala Leu Ala Asp Pro Asn Trp Leu Arg Arg Gln  
 530 535 540

Val Gly Val Val Leu Gln Asp Asn Val Leu Leu Asn Arg Ser Ile Ile  
 545 550 555 560

Asp Asn Ile Ser Leu Ala Asn Pro Gly Met Ser Val Glu Lys Val Ile  
 565 570 575

Tyr Ala Ala Lys Leu Ala Gly Ala His Asp Phe Ile Ser Glu Leu Arg  
 580 585 590

Glu Gly Tyr Asn Thr Ile Val Gly Glu Gln Gly Ala Gly Leu Ser Gly  
 595 600 605

Gly Gln Arg Gln Arg Ile Ala Ile Ala Arg Ala Leu Val Asn Asn Pro  
 610 615 620

Lys Ile Leu Ile Phe Asp Glu Ala Thr Ser Ala Leu Asp Tyr Glu Ser  
 625 630 635 640

Glu His Ile Ile Met Arg Asn Met His Lys Ile Cys Lys Gly Arg Thr  
 645 650 655

Val Ile Ile Ile Ala His Arg Leu Ser Thr Val Lys Asn Ala Asp Arg  
 660 665 670

Ile Ile Val Met Glu Lys Gly Lys Ile Val Glu Gln Gly Lys His Lys  
 675 680 685

Glu Leu Leu Ser Glu Pro Glu Ser Leu Tyr Ser Tyr Leu Tyr Gln Leu  
 690 695 700

Gln Ser Asp  
 705

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 <212> DNA  
 <213> Artificial Sequence

<220>  
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<400> 22  
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<210> 23  
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 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<220>  
 <221> modified\_base  
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<400> 23  
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<210> 24  
 <211> 32  
 <212> DNA  
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<220>  
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<220>  
 <221> modified\_base  
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<400> 24  
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32

<210> 25  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence

<220>  
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 <223> a, t, c, g, other or unknown

<220>  
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 <222> (18)  
 <223> a, t, c, g, other or unknown

<220>  
 <221> modified\_base  
 <222> (24)  
 <223> a, t, c, g, other or unknown

<400> 25  
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27

<210> 26  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 26  
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26

<210> 27  
 <211> 35  
 <212> DNA  
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<220>  
 <223> Description of Artificial Sequence: Primer

<400> 27  
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35

<210> 28  
 <211> 30

<212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 28  
 atcactatgtt ccataatcta taaccaatga

30

<210> 29  
 <211> 9  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: consensus  
 sequence

<220>  
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 <222> (1)..(2)  
 <223> Any amino acid

<220>  
 <221> MOD\_RES  
 <222> (5)  
 <223> Any amino acid

<220>  
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<220>  
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<400> 29  
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<210> 30  
 <211> 2215  
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<220>  
 <221> CDS  
 <222> (1)..(2211)

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 1 5 10 15

agt aat tta gtt atg ata gat tat gct caa caa cct gct cta tct gct	96
Ser Asn Leu Val Met Ile Asp Tyr Ala Gln Gln Pro Ala Leu Ser Ala	
20 25 30	
ctg gtt atc ctt gcc aaa tac tat ggt att tct gca agt cca gca gac	144
Leu Val Ile Leu Ala Lys Tyr Tyr Gly Ile Ser Ala Ser Pro Ala Asp	
35 40 45	
att atg cat cag ttt tct gat aat aca aaa gga gac ctg aat gaa att	192
Ile Met His Gln Phe Ser Asp Asn Thr Lys Gly Asp Leu Asn Glu Ile	
50 55 60	
gaa tgg atg ttg gca gca aag aaa tta gaa tta aag gta aag att ata	240
Glu Trp Met Leu Ala Ala Lys Lys Leu Glu Leu Lys Val Lys Ile Ile	
65 70 75 80	
aaa cag cct tta act cga ttg tca atg ata aca ctt cct gct ttg gtg	288
Lys Gln Pro Leu Thr Arg Leu Ser Met Ile Thr Leu Pro Ala Leu Val	
85 90 95	
tgg tgt gat aat aag ccc gat tta gat caa aat tta aac tct cat ttt	336
Trp Cys Asp Asn Lys Pro Asp Leu Asp Gln Asn Leu Asn Ser His Phe	
100 105 110	
ata cta act aaa att gat ggg gtg gga tct gct gca aaa tat ctc atc	384
Ile Leu Thr Lys Ile Asp Gly Val Gly Ser Ala Ala Lys Tyr Leu Ile	
115 120 125	
tac gat ttg att gag aat cgt ccc ata ata tta gat gca agt gag ttt	432
Tyr Asp Leu Ile Glu Asn Arg Pro Ile Ile Leu Asp Ala Ser Glu Phe	
130 135 140	
tct gaa aga tat tct ggt aag tta atg cta gta act tcc cgt gcg tca	480
Ser Glu Arg Tyr Ser Gly Lys Leu Met Leu Val Thr Ser Arg Ala Ser	
145 150 155 160	
ata ttg ggt tca ttg gct aaa ttt gat ttt act tgg ttt att cct gcg	528
Ile Leu Gly Ser Leu Ala Lys Phe Asp Phe Thr Trp Phe Ile Pro Ala	
165 170 175	
gta atc aaa tat cgt tat att ttt ttt gaa gtc atc gtt att tca gtg	576
Val Ile Lys Tyr Arg Tyr Ile Phe Phe Glu Val Ile Val Ile Ser Val	
180 185 190	
gtg cta cag att ttt gct ctg att acg cca ttg ttt ttt cag gtt gtg	624
Val Leu Gln Ile Phe Ala Leu Ile Thr Pro Leu Phe Phe Gln Val Val	
195 200 205	
atg gat aag gta ttg gtg cat cgt ggt ttt tct act ctg gat gtg gta	672
Met Asp Lys Val Leu Val His Arg Gly Phe Ser Thr Leu Asp Val Val	
210 215 220	
gcg att gcc ttg ttg gta gta agt tta ttt gaa gtc att tta agt ggt	720
Ala Ile Ala Leu Leu Val Val Ser Leu Phe Glu Val Ile Leu Ser Gly	
225 230 235 240	

ctc cgc act tat att ttt gct cat aca acc tct cga att gat gta gag	768
Leu Arg Thr Tyr Ile Phe Ala His Thr Thr Ser Arg Ile Asp Val Glu	
245 250 255	
ctc gga gca cga tta ttt cgt cat cta tta gct cta ccg ctt gct tat	816
Leu Gly Ala Arg Leu Phe Arg His Leu Leu Ala Leu Pro Leu Ala Tyr	
260 265 270	
ttt gag agt aga aga gta ggc gat aca gtt gca cgt ata cgt gaa ttg	864
Phe Glu Ser Arg Arg Val Gly Asp Thr Val Ala Arg Ile Arg Glu Leu	
275 280 285	
gaa cat atc cgc aat ttc tta act ggt caa gct ctc act tca gtt tta	912
Glu His Ile Arg Asn Phe Leu Thr Gly Gln Ala Leu Thr Ser Val Leu	
290 295 300	
gat ttg gtg ttt tct ttt ata ttc ttg ttt gta atg tgg tat tac agc	960
Asp Leu Val Phe Ser Phe Ile Phe Leu Phe Val Met Trp Tyr Tyr Ser	
305 310 315 320	
cct act tta aca ctg gta gtt ttg gca tca tta cca ata tat gcg ttt	1008
Pro Thr Leu Thr Leu Val Val Leu Ala Ser Leu Pro Ile Tyr Ala Phe	
325 330 335	
tgg tct gcc ttt att agc cca att tta cgc act cga cta aat gat caa	1056
Trp Ser Ala Phe Ile Ser Pro Ile Leu Arg Thr Arg Leu Asn Asp Gln	
340 345 350	
ttt gca cgc aat gca gat aat caa tct ttt tta gtg gaa agt att act	1104
Phe Ala Arg Asn Ala Asp Asn Gln Ser Phe Leu Val Glu Ser Ile Thr	
355 360 365	
gcg gtt ggt acg gta aaa gca atg gca gtt gaa cct caa atg acc cgt	1152
Ala Val Gly Thr Val Lys Ala Met Ala Val Glu Pro Gln Met Thr Arg	
370 375 380	
cgc tgg gat aat caa tta gca gct tat gtg gtt tct agt ttt cgg gta	1200
Arg Trp Asp Asn Gln Leu Ala Ala Tyr Val Val Ser Ser Phe Arg Val	
385 390 395 400	
gct aag ttg gca atg gtt ggg cag caa gga gta caa ctc att caa aag	1248
Ala Lys Leu Ala Met Val Gly Gln Gln Gly Val Gln Leu Ile Gln Lys	
405 410 415	
atg gtt att gtg gca act cta tgg att ggt gca aaa ttg gta att gaa	1296
Met Val Ile Val Ala Thr Leu Trp Ile Gly Ala Lys Leu Val Ile Glu	
420 425 430	
ggc aag cta tcg gta ggt caa tta ata gca ttt aat atg ctg gca ggt	1344
Gly Lys Leu Ser Val Gly Gln Leu Ile Ala Phe Asn Met Leu Ala Gly	
435 440 445	
cag gtg gcc gct cct gtt atc cgc ctg gca cag cta tgg caa gat ttt	1392
Gln Val Ala Ala Pro Val Ile Arg Leu Ala Gln Leu Trp Gln Asp Phe	
450 455 460	

cag caa gta ggt att tca gtg gcg aga ttg ggt gat att tta aat act Gln Gln Val Gly Ile Ser Val Ala Arg Leu Gly Asp Ile Leu Asn Thr 465 470 475 480	1440
cca act gag cat tct aca tct cgc tta act tta cct gat att aag ggt Pro Thr Glu His Ser Thr Ser Arg Leu Thr Leu Pro Asp Ile Lys Gly 485 490 495	1488
gat att aca ttt gaa aat gtt gat ttt cgc tac aaa ata gat ggg cat Asp Ile Thr Phe Glu Asn Val Asp Phe Arg Tyr Lys Ile Asp Gly His 500 505 510	1536
tta ata tta cag aat tta aat tta cag att aac gct gga gag ata cta Leu Ile Leu Gln Asn Leu Asn Leu Gln Ile Asn Ala Gly Glu Ile Leu 515 520 525	1584
ggt atc gta gga cgc tct ggt tca ggt aaa tca aca ttg aca aaa tta Gly Ile Val Gly Arg Ser Gly Ser Gly Lys Ser Thr Leu Thr Lys Leu 530 535 540	1632
gta cag cgt tta tat gta cca gaa aat ggg cga ata tta gtt gat gga Val Gln Arg Leu Tyr Val Pro Glu Asn Gly Arg Ile Leu Val Asp Gly 545 550 555 560	1680
aac gat ttg gca tta gct gat ccc gct tgg ctg cgt cgc caa gtg ggt Asn Asp Leu Ala Leu Ala Asp Pro Ala Trp Leu Arg Arg Gln Val Gly 565 570 575	1728
gtt gtt ttg cag gaa aat gtg tta ctc aat cgt agt att cga gat aat Val Val Leu Gln Glu Asn Val Leu Leu Asn Arg Ser Ile Arg Asp Asn 580 585 590	1776
att gcc cta act gat acg ggc atg tca tta gag ttt att atc cag gct Ile Ala Leu Thr Asp Thr Gly Met Ser Leu Glu Phe Ile Ile/Gln Ala 595 600 605	1824
gcc aag atg tct ggg gca cat gac ttt att atg gaa ttg cct gag ggt Ala Lys Met Ser Gly Ala His Asp Phe Ile Met Glu Leu Pro Glu Gly 610 615 620	1872
tat gat acg att gtt gga gag caa ggt gca ggc ttg tca ggt gga caa Tyr Asp Thr Ile Val Gly Glu Gln Gly Ala Gly Leu Ser Gly Gly Gln 625 630 635 640	1920
cgc cag cgt atc gct att gcg cgt gct tta att acc aat ccg cgt att Arg Gln Arg Ile Ala Ile Ala Arg Ala Leu Ile Thr Asn Pro Arg Ile 645 650 655	1968
ttg att ttt gat gaa gct act agt gca tta gac tat gag tcg gaa agg Leu Ile Phe Asp Glu Ala Thr Ser Ala Leu Asp Tyr Glu Ser Glu Arg 660 665 670	2016
gct att atg caa aat atg cag gca att tgc caa ggt aga aca gca ttg Ala Ile Met Gln Asn Met Gln Ala Ile Cys Gln Gly Arg Thr Val Leu 675 680 685	2064

att att gca cat cgc tta tct acc gta aaa atg gca cat cgc att att	2112
Ile Ile Ala His Arg Leu Ser Thr Val Lys Met Ala His Arg Ile Ile	
690 695 700	
gca atg gac aag ggg aaa att gta gag caa ggc aca cat caa gaa ttg	2160
Ala Met Asp Lys Gly Lys Ile Val Glu Gln Gly Thr His Gln Glu Leu	
705 710 715 720	
ttg caa aaa gaa gat ggt tac tat cgt tat tta tat gat ttg cag aat	2208
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gga taaa	2215
Gly	
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<220>	
<221> CDS	
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1 5 10 15	
aac tct gat atg cat aaa cat tgg acg ttg tct ttg ttt gcg acc aat	96
Asn Ser Asp Met His Lys His Trp Thr Leu Ser Leu Phe Ala Thr Asn	
20 25 30	
gtt att ccg gca att gag aca ggt caa tat gtt ata ttg aaa aga gaa	144
Val Ile Pro Ala Ile Glu Thr Gly Gln Tyr Val Ile Leu Lys Arg Glu	
35 40 45	
gat atg cct gta gca tat tgt agt tgg gct aaa ctt agt tta gaa aac	192
Asp Met Pro Val Ala Tyr Cys Ser Trp Ala Lys Leu Ser Leu Glu Asn	
50 55 60	
gag gtt aaa tat att aac gat gtt act tct ctt aag tta gat gac tgg	240
Glu Val Lys Tyr Ile Asn Asp Val Thr Ser Leu Lys Leu Asp Asp Trp	
65 70 75 80	
cag tca ggt gac cga aac tgg ttt att gac tgg att gct cca ttt ggc	288
Gln Ser Gly Asp Arg Asn Trp Phe Ile Asp Trp Ile Ala Pro Phe Gly	
85 90 95	
gat agt ctt aca ctc aca aaa cac atg aga acg tta ttt tca gat gaa	336
Asp Ser Leu Thr Leu Thr Lys His Met Arg Thr Leu Phe Ser Asp Glu	
100 105 110	
ttg ttt aga gcg att cgt gta gat gga aat tca tcg cat ggt aag ata	384
Leu Phe Arg Ala Ile Arg Val Asp Gly Asn Ser Ser His Gly Lys Ile	
115 120 125	

tct gaa ttt tat gga aag tct gtt gat tca aaa tta gcc tca aga ata	432																
Ser Glu Phe Tyr Gly Lys Ser Val Asp Ser Lys Leu Ala Ser Arg Ile																	
130	135		140	ttt gca caa tat cac gaa gat ttg acg agc aaa ttg tca act cag aat	480	Phe Ala Gln Tyr His Glu Asp Leu Thr Ser Lys Leu Ser Thr Gln Asn		145	150		155	aat ttt att ata tct aaa gat aat taa	507	Asn Phe Ile Ile Ser Lys Asp Asn		165	
	140																
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Phe Ala Gln Tyr His Glu Asp Leu Thr Ser Lys Leu Ser Thr Gln Asn																	
145	150		155	aat ttt att ata tct aaa gat aat taa	507	Asn Phe Ile Ile Ser Lys Asp Asn		165									
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<400> 32																																																									
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	10	15																																																							
Asn Ser Asp Met His Lys His Trp Thr Leu Ser Leu Phe Ala Thr Asn																																																									
20	25	30																																																							
Val Ile Pro Ala Ile Glu Thr Gly Gln Tyr Val Ile Leu Lys Arg Glu																																																									
35	40	45																																																							
Asp Met Pro Val Ala Tyr Cys Ser Trp Ala Lys Leu Ser Leu Glu Asn																																																									
50	55	60																																																							
Glu Val Lys Tyr Ile Asn Asp Val Thr Ser Leu Lys Leu Asp Asp Trp																																																									
65	70		75	80	Gln Ser Gly Asp Arg Asn Trp Phe Ile Asp Trp Ile Ala Pro Phe Gly		85	90	95	Asp Ser Leu Thr Leu Thr Lys His Met Arg Thr Leu Phe Ser Asp Glu		100	105	110	Leu Phe Arg Ala Ile Arg Val Asp Gly Asn Ser Ser His Gly Lys Ile		115	120	125	Ser Glu Phe Tyr Gly Lys Ser Val Asp Ser Lys Leu Ala Ser Arg Ile		130	135	140	Phe Ala Gln Tyr His Glu Asp Leu Thr Ser Lys Leu Ser Thr Gln Asn		145	150		155	160	Asn Phe Ile Ile Ser Lys Asp Asn		165																							
	75	80																																																							
Gln Ser Gly Asp Arg Asn Trp Phe Ile Asp Trp Ile Ala Pro Phe Gly																																																									
85	90	95																																																							
Asp Ser Leu Thr Leu Thr Lys His Met Arg Thr Leu Phe Ser Asp Glu																																																									
100	105	110																																																							
Leu Phe Arg Ala Ile Arg Val Asp Gly Asn Ser Ser His Gly Lys Ile																																																									
115	120	125																																																							
Ser Glu Phe Tyr Gly Lys Ser Val Asp Ser Lys Leu Ala Ser Arg Ile																																																									
130	135	140																																																							
Phe Ala Gln Tyr His Glu Asp Leu Thr Ser Lys Leu Ser Thr Gln Asn																																																									
145	150		155	160	Asn Phe Ile Ile Ser Lys Asp Asn		165																																																		
	155	160																																																							
Asn Phe Ile Ile Ser Lys Asp Asn																																																									
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<210> 33  
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 <212> PRT  
 <213> Pasteurella haemolytica

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 20 25 30  
 Asn Val Ile Pro Ala Ile Glu Asn Glu Gln Tyr Met Leu Leu Ile Asp  
 35 40 45  
 Asn Gly Ile Pro Ile Ala Tyr Cys Ser Trp Ala Asp Leu Asn Leu Glu  
 50 55 60  
 Thr Glu Val Lys Tyr Ile Lys Asp Ile Asn Ser Leu Thr Pro Glu Glu  
 65 70 75 80  
 Trp Gln Ser Gly Asp Arg Arg Trp Ile Ile Asp Trp Val Ala Pro Phe  
 85 90 95  
 Gly His Ser Gln Leu Leu Tyr Lys Lys Met Cys Gln Lys Tyr Pro Asp  
 100 105 110  
 Met Ile Val Arg Ser Ile Arg Phe Tyr Pro Lys Gln Lys Glu Leu Gly  
 115 120 125  
 Lys Ile Ala Tyr Phe Lys Gly Gly Lys Leu Asp Lys Lys Thr Ala Lys  
 130 135 140  
 Lys Arg Phe Asp Thr Tyr Gln Glu Glu Leu Ala Thr Ala Leu Lys Asn  
 145 150 155 160  
 Glu Phe Asn Phe Ile Lys Lys  
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<210> 34  
<211> 172  
<212> PRT  
<213> *Actinobacillus pleuropneumoniae*

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<400> 34
Met Ser Lys Lys Ile Asn Gly Phe Glu Val Leu Gly Glu Val Ala Trp
  1           5           10           15

Leu Trp Ala Ser Ser Pro Leu His Arg Lys Trp Pro Leu Ser Leu Leu
  20          25          30

Ala Ile Asn Val Leu Pro Ala Ile Glu Ser Asn Gln Tyr Val Leu Leu
  35          40          45

Lys Arg Asp Gly Phe Pro Ile Ala Phe Cys Ser Trp Ala Asn Leu Asn
  50          55          60

Leu Glu Asn Glu Ile Lys Tyr Leu Asp Asp Val Ala Ser Leu Val Ala
  65          70          75          80

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Asp Asp Trp Thr Ser Gly Asp Arg Arg Trp Phe Ile Asp Trp Ile Ala  
 85 90 95

Pro Phe Gly Asp Ser Ala Ala Leu Tyr Lys His Met Arg Asp Asn Phe  
 100 105 110

Pro Asn Glu Leu Phe Arg Ala Ile Arg Val Asp Pro Asp Ser Arg Val  
 115 120 125

Gly Lys Ile Ser Glu Phe His Gly Gly Lys Ile Asp Lys Lys Leu Ala  
 130 135 140

Ser Lys Ile Phe Gln Gln Tyr His Phe Glu Leu Met Ser Glu Leu Lys  
 145 150 155 160

Asn Lys Gln Asn Phe Lys Phe Ser Leu Val Asn Ser  
 165 170

<210> 35

<211> 170

<212> PRT

<213> Escherichia coli

<400> 35

Met Asn Arg Asn Asn Pro Leu Glu Val Leu Gly His Val Ser Trp Leu  
 1 5 10 15

Trp Ala Ser Ser Pro Leu His Arg Asn Trp Pro Val Ser Leu Phe Ala  
 20 25 30

Ile Asn Val Leu Pro Ala Ile Arg Ala Asn Gln Tyr Ala Leu Leu Thr  
 35 40 45

Arg Asp Asn Tyr Pro Val Ala Tyr Cys Ser Trp Ala Asn Leu Ser Leu  
 50 55 60

Glu Asn Glu Ile Lys Tyr Leu Asn Asp Val Thr Ser Leu Val Ala Glu  
 65 70 75 80

Asp Trp Thr Ser Gly Asp Arg Lys Trp Phe Ile Val Trp Ile Ala Pro  
 85 90 95

Phe Gly Asp Asn Gly Ala Leu Tyr Lys Tyr Met Arg Lys Lys Phe Pro  
 100 105 110

Asp Glu Leu Phe Arg Ala Ile Arg Val Asp Pro Lys Thr His Val Gly  
 115 120 125

Lys Val Ser Glu Phe His Gly Gly Lys Ile Asp Lys Gln Leu Ala Asn  
 130 135 140

Lys Ile Phe Lys Gln Tyr His His Glu Leu Ile Thr Glu Val Lys Asn  
 145 150 155 160

Lys Ser Asp Phe Asn Phe Ser Leu Thr Gly  
 165 170

<210> 36  
 <211> 1428  
 <212> DNA  
 <213> *Moraxella bovis*

<220>  
 <221> CDS  
 <222> (1)..(1425)

<400> 36  
 atg ttt ata caa gca ctt aaa gat ttt ttt att cgc tat ata acc gtt 48  
 Met Phe Ile Gln Ala Leu Lys Asp Phe Phe Ile Arg Tyr Ile Thr Val  
 1 5 10 15

tgg cgc aat aca tgg gca gtt cga gac caa cta acc cct cct aag cgt 96  
 Trp Arg Asn Thr Trp Ala Val Arg Asp Gln Leu Thr Pro Pro Lys Arg  
 20 25 30

act aaa gaa gaa ctc gct ttt ctt cct gca cat cta gaa ctc act gac 144  
 Thr Lys Glu Glu Leu Ala Phe Leu Pro Ala His Leu Glu Leu Thr Asp  
 35 40 45

aca cct gta tcc aga tct tct aag tgg aca gct aga ata atc atg ata 192  
 Thr Pro Val Ser Arg Ser Ser Lys Trp Thr Ala Arg Ile Ile Met Ile  
 50 55 60

ttt gtc cta ttt gct ttg cta tgg tct tgg gtt gga cag att gac att 240  
 Phe Val Leu Phe Ala Leu Leu Trp Ser Trp Val Gly Gln Ile Asp Ile  
 65 70 75 80

gtt gct aca gct tca ggt aaa att tct tca ggt agc cgt agc aag act 288  
 Val Ala Thr Ala Ser Gly Lys Ile Ser Ser Gly Ser Arg Ser Lys Thr  
 85 90 95

att caa tct ttg gaa aca gcg ata gtt aaa gca gtt tat gta cgt gat 336  
 Ile Gln Ser Leu Glu Thr Ala Ile Val Lys Ala Val Tyr Val Arg Asp  
 100 105 110

ggt caa aat gtt caa caa ggt gaa ata tta gta gat tta gtg gga atc 384  
 Gly Gln Asn Val Gln Gln Gly Glu Ile Leu Val Asp Leu Val Gly Ile  
 115 120 125

ggt tca gat agt gat gtt gct cag tcc gag aaa gcc ctt cga gca gcg 432  
 Gly Ser Asp Ser Asp Val Ala Gln Ser Glu Lys Ala Leu Arg Ala Ala  
 130 135 140

caa tta tct aag cta cgc ctt gaa gca att tta tca gca tta aat cac 480  
 Gln Leu Ser Lys Leu Arg Leu Glu Ala Ile Leu Ser Ala Leu Asn His  
 145 150 155 160

cgt att aat cct cag att gat gta gca tat gca aag tct tta aat att 528  
 Arg Ile Asn Pro Gln Ile Asp Val Ala Tyr Ala Lys Ser Leu Asn Ile  
 165 170 175

tca gaa tcg gaa att aat gaa gct caa act tta gcc caa aat caa tat 576  
 Ser Glu Ser Glu Ile Asn Glu Ala Gln Thr Leu Ala Gln Asn Gln Tyr  
 180 185 190

caa gca tgg tta gca caa gat gaa caa cta aaa tta acc tta aaa gga	624
Gln Ala Trp Leu Ala Gln Asp Glu Gln Leu Lys Leu Thr Leu Lys Gly	
195 200 205	
cat caa gca gaa tta caa tct gct cga tcc caa gaa caa aag ttg gtt	672
His Gln Ala Glu Leu Gln Ser Ala Arg Ser Gln Glu Gln Lys Leu Val	
210 215 220	
tca gtt ggt gca att gaa cat caa aag act gat gat tat cgg agt ctc	720
Ser Val Gly Ala Ile Glu His Gln Lys Thr Asp Asp Tyr Arg Ser Leu	
225 230 235 240	
aaa gca gaa aat ttt ata tct gag cat gct tat cta gaa caa gaa agc	768
Lys Ala Glu Asn Phe Ile Ser Glu His Ala Tyr Leu Glu Gln Glu Ser	
245 250 255	
aaa tta ctt agc aat caa aat gat tta caa agt aca cgt agt cag att	816
Lys Leu Leu Ser Asn Gln Asn Asp Leu Gln Ser Thr Arg Ser Gln Ile	
260 265 270	
caa aaa ata cag gct gca atc atg caa gct gaa cag aac cgt atg tta	864
Gln Lys Ile Gln Ala Ala Ile Met Gln Ala Glu Gln Asn Arg Met Leu	
275 280 285	
tat act caa aat cta aaa cgt gat aca tta gaa tct tta cgc caa acc	912
Tyr Thr Gln Asn Leu Lys Arg Asp Thr Leu Glu Ser Leu Arg Gln Thr	
290 295 300	
aat gaa cag att aat caa tat act ggt caa act aat aaa gct aag cag	960
Asn Glu Gln Ile Asn Gln Tyr Thr Gly Gln Thr Asn Lys Ala Lys Gln	
305 310 315 320	
cga cag aaa ttg ctg agt att aaa tca cct gtt aat ggt act ata caa	1008
Arg Gln Lys Leu Leu Ser Ile Lys Ser Pro Val Asn Gly Thr Ile Gln	
325 330 335	
gag cta aca gct tat act tta ggt gga gtt gta caa gca gca caa aaa	1056
Glu Leu Thr Ala Tyr Thr Leu Gly Gly Val Val Gln Ala Ala Gln Lys	
340 345 350	
att atg gtt gtg gca cct aac gat aat caa gtg gaa gta gag gta tta	1104
Ile Met Val Val Ala Pro Asn Asp Asn Gln Val Glu Val Glu Val Leu	
355 360 365	
gtg cta aat aaa gat atc ggc ttt gta aaa gct ggg cag aat gtt atc	1152
Val Leu Asn Lys Asp Ile Gly Phe Val Lys Ala Gly Gln Asn Val Ile	
370 375 380	
atc aaa atc gag agt ttt cct tat aca cgt tat ggt tat tta aca ggt	1200
Ile Lys Ile Glu Ser Phe Pro Tyr Thr Arg Tyr Gly Tyr Leu Thr Gly	
385 390 395 400	
aaa ata aaa agt att agt cat gat gct ata gaa cat caa cat tta ggt	1248
Lys Ile Lys Ser Ile Ser His Asp Ala Ile Glu His Gln His Leu Gly	
405 410 415	

ctg	gtg	tat	act	gca	ctt	gtt	tct	ctt	gat	aaa	agc	aca	tta	aat	ata	1296
Leu	Val	Tyr	Thr	Ala	Leu	Val	Ser	Leu	Asp	Lys	Ser	Thr	Leu	Asn	Ile	
420								425					430			
gat	gga	gta	aca	atc	aac	tta	acg	cca	gga	atg	aat	gtt	act	gct	gaa	1344
Asp	Gly	Val	Thr	Ile	Asn	Leu	Thr	Pro	Gly	Met	Asn	Val	Thr	Ala	Glu	
435							440					445				
att	aaa	aca	ggt	aaa	cgt	cgt	gtt	ttg	gat	tat	ata	tta	agt	cca	ttg	1392
Ile	Lys	Thr	Gly	Lys	Arg	Arg	Val	Leu	Asp	Tyr	Ile	Leu	Ser	Pro	Leu	
450							455				460					
cag	aca	aaa	gtt	gat	gaa	agt	ttt	cga	gaa	cgc	taa					1428
Gln	Thr	Lys	Val	Asp	Glu	Ser	Phe	Arg	Glu	Arg						
465					470				475							
<210> 37																
<211> 475																
<212> PRT																
<213> Moraxella bovis																
<400> 37																
Met	Phe	Ile	Gln	Ala	Leu	Lys	Asp	Phe	Phe	Ile	Arg	Tyr	Ile	Thr	Val	
1					5				10				15			
Trp	Arg	Asn	Thr	Trp	Ala	Val	Arg	Asp	Gln	Leu	Thr	Pro	Pro	Lys	Arg	
					20			25				30				
Thr	Lys	Glu	Glu	Leu	Ala	Phe	Leu	Pro	Ala	His	Leu	Glu	Leu	Thr	Asp	
					35			40			45					
Thr	Pro	Val	Ser	Arg	Ser	Ser	Lys	Trp	Thr	Ala	Arg	Ile	Ile	Met	Ile	
					50			55			60					
Phe	Val	Leu	Phe	Ala	Leu	Leu	Trp	Ser	Trp	Val	Gly	Gln	Ile	Asp	Ile	
					65			70			75			80		
Val	Ala	Thr	Ala	Ser	Gly	Lys	Ile	Ser	Ser	Gly	Ser	Arg	Ser	Lys	Thr	
					85			90			95					
Ile	Gln	Ser	Leu	Glu	Thr	Ala	Ile	Val	Lys	Ala	Val	Tyr	Val	Arg	Asp	
					100			105			110					
Gly	Gln	Asn	Val	Gln	Gln	Gly	Glu	Ile	Leu	Val	Asp	Leu	Val	Gly	Ile	
					115			120			125					
Gly	Ser	Asp	Ser	Asp	Val	Ala	Gln	Ser	Glu	Lys	Ala	Leu	Arg	Ala	Ala	
					130			135			140					
Gln	Leu	Ser	Lys	Leu	Arg	Leu	Glu	Ala	Ile	Leu	Ser	Ala	Leu	Asn	His	
					145			150			155			160		
Arg	Ile	Asn	Pro	Gln	Ile	Asp	Val	Ala	Tyr	Ala	Lys	Ser	Leu	Asn	Ile	
					165			170			175					
Ser	Glu	Ser	Glu	Ile	Asn	Glu	Ala	Gln	Thr	Leu	Ala	Gln	Asn	Gln	Tyr	
					180			185			190					

Gln Ala Trp Leu Ala Gln Asp Glu Gln Leu Lys Leu Thr Leu Lys Gly  
 195 200 205

His Gln Ala Glu Leu Gln Ser Ala Arg Ser Gln Glu Gln Lys Leu Val  
 210 215 220

Ser Val Gly Ala Ile Glu His Gln Lys Thr Asp Asp Tyr Arg Ser Leu  
 225 230 235 240

Lys Ala Glu Asn Phe Ile Ser Glu His Ala Tyr Leu Glu Gln Glu Ser  
 245 250 255

Lys Leu Leu Ser Asn Gln Asn Asp Leu Gln Ser Thr Arg Ser Gln Ile  
 260 265 270

Gln Lys Ile Gln Ala Ala Ile Met Gln Ala Glu Gln Asn Arg Met Leu  
 275 280 285

Tyr Thr Gln Asn Leu Lys Arg Asp Thr Leu Glu Ser Leu Arg Gln Thr  
 290 295 300

Asn Glu Gln Ile Asn Gln Tyr Thr Gly Gln Thr Asn Lys Ala Lys Gln  
 305 310 315 320

Arg Gln Lys Leu Leu Ser Ile Lys Ser Pro Val Asn Gly Thr Ile Gln  
 325 330 335

Glu Leu Thr Ala Tyr Thr Leu Gly Gly Val Val Gln Ala Ala Gln Lys  
 340 345 350

Ile Met Val Val Ala Pro Asn Asp Asn Gln Val Glu Val Glu Val Leu  
 355 360 365

Val Leu Asn Lys Asp Ile Gly Phe Val Lys Ala Gly Gln Asn Val Ile  
 370 375 380

Ile Lys Ile Glu Ser Phe Pro Tyr Thr Arg Tyr Gly Tyr Leu Thr Gly  
 385 390 395 400

Lys Ile Lys Ser Ile Ser His Asp Ala Ile Glu His Gln His Leu Gly  
 405 410 415

Leu Val Tyr Thr Ala Leu Val Ser Leu Asp Lys Ser Thr Leu Asn Ile  
 420 425 430

Asp Gly Val Thr Ile Asn Leu Thr Pro Gly Met Asn Val Thr Ala Glu  
 435 440 445

Ile Lys Thr Gly Lys Arg Arg Val Leu Asp Tyr Ile Leu Ser Pro Leu  
 450 455 460

Gln Thr Lys Val Asp Glu Ser Phe Arg Glu Arg  
 465 470 475

<210> 38  
 <211> 478  
 <212> PRT  
 <213> Pasteurella haemolytica

<400> 38  
 Met Lys Ile Trp Leu Ser Gly Ile Tyr Glu Phe Phe Leu Arg Tyr Lys  
 1 5 10 15  
 Asn Ile Trp Ala Glu Val Trp Lys Ile Arg Lys Glu Leu Asp His Pro  
 20 25 30  
 Asn Arg Lys Lys Asp Glu Ser Glu Phe Leu Pro Ala His Leu Glu Leu  
 35 40 45  
 Ile Glu Thr Pro Val Ser Lys Lys Pro Arg Leu Ile Ala Tyr Leu Ile  
 50 55 60  
 Met Leu Phe Leu Val Val Ala Ile Val Leu Ala Ser Val Ser Lys Val  
 65 70 75 80  
 Glu Ile Val Ala Thr Ala Pro Gly Lys Leu Thr Phe Ser Gly Arg Ser  
 85 90 95  
 Lys Glu Ile Lys Pro Ile Glu Asn Ala Ile Val Gln Glu Ile Phe Val  
 100 105 110  
 Lys Asp Gly Gln Phe Val Glu Lys Gly Gln Leu Leu Val Ser Leu Thr  
 115 120 125  
 Ala Leu Gly Ser Asp Ala Asp Ile Lys Lys Thr Met Ala Ser Leu Ser  
 130 135 140  
 Leu Ala Lys Leu Glu Asn Tyr Arg Tyr Gln Thr Leu Leu Thr Ala Ile  
 145 150 155 160  
 Glu Lys Glu Ser Leu Pro Val Ile Asp Leu Ser Arg Thr Glu Phe Lys  
 165 170 175  
 Asp Ser Ser Glu Glu Asp Arg Leu Arg Ile Lys His Leu Ile Glu Glu  
 180 185 190  
 Gln Tyr Thr Thr Trp Gln Lys Gln Lys Thr Gln Lys Thr Leu Ala Tyr  
 195 200 205  
 Lys Arg Lys Glu Ala Glu Lys Gln Thr Ile Phe Ala Tyr Val Arg Lys  
 210 215 220  
 Tyr Glu Gly Ala Thr Arg Ile Glu Gln Glu Lys Leu Lys Asp Phe Lys  
 225 230 235 240  
 Ala Leu Tyr Lys Gln Lys Ser Leu Ser Lys His Glu Leu Leu Ala Gln  
 245 250 255  
 Glu Asn Lys Leu Ile Glu Ala Gln Asn Ala Val Ala Val Tyr Arg Ser  
 260 265 270

Lys Leu Asn Glu Leu Glu Asn Asp Leu Leu Asn Val Lys Glu Glu Leu  
 275 280 285

Glu Leu Ile Thr Gln Phe Phe Lys Ser Asp Val Leu Glu Lys Leu Lys  
 290 295 300

Gln His Ile Glu Asn Glu Arg Gln Leu Arg Leu Glu Leu Glu Lys Asn  
 305 310 315 320

Asn Gln Arg Arg Gln Ala Ser Met Ile Arg Ala Pro Val Ser Gly Thr  
 325 330 335

Val Gln Gln Leu Lys Ile His Thr Ile Gly Gly Val Val Thr Thr Ala  
 340 345 350

Glu Thr Leu Met Ile Ile Val Pro Glu Asp Asp Val Leu Glu Ala Thr  
 355 360 365

Ala Leu Val Pro Asn Lys Asp Ile Gly Phe Val Ala Ala Gly Gln Glu  
 370 375 380

Val Ile Ile Lys Val Glu Thr Phe Pro Tyr Thr Arg Tyr Gly Tyr Leu  
 385 390 395 400

Thr Gly Arg Ile Lys His Ile Ser Pro Asp Ala Ile Glu Gln Pro Asn  
 405 410 415

Val Gly Leu Val Phe Asn Ala Thr Ile Ala Ile Asp Arg Lys Asn Leu  
 420 425 430

Thr Ser Pro Asp Gly Arg Lys Ile Asp Leu Ser Ser Gly Met Thr Ile  
 435 440 445

Thr Ala Glu Ile Lys Thr Gly Glu Arg Ser Val Met Ser Tyr Leu Leu  
 450 455 460

Ser Pro Leu Glu Glu Ser Val Thr Glu Ser Leu Arg Glu Arg  
 465 470 475

<210> 39  
 <211> 478  
 <212> PRT  
 <213> *Actinobacillus pleuropneumoniae*

<400> 39  
 Met Lys Thr Trp Leu Met Gly Leu Tyr Glu Phe Phe Gln Arg Tyr Lys  
 1 5 10 15

Thr Val Trp Thr Glu Ile Trp Lys Ile Arg His Gln Leu Asp Thr Pro  
 20 25 30

Asp Arg Glu Lys Asp Glu Asn Glu Phe Leu Pro Ala His Leu Glu Leu  
 35 40 45

Ile Glu Thr Pro Val Ser Lys Lys Pro Arg Leu Ile Ala Tyr Leu Ile  
 50 55 60

Met Leu Phe Leu Phe Leu Ala Leu Val Ile Ser Ile Val Ser His Val  
 65 70 75 80  
 Glu Ile Val Ala Thr Ala Thr Gly Lys Leu Ala Phe Ser Asp Arg Ser  
 85 90 95  
 Lys Glu Ile Lys Pro Ile Glu Asn Ala Leu Val Lys Glu Ile Phe Val  
 100 105 110  
 Gln Asp Gly Gln Phe Val Glu Lys Asp Gln Leu Leu Leu His Leu Thr  
 115 120 125  
 Ala Leu Gly Ala Asp Ala Asp Gln Gln Lys Thr Lys Ser Ser Leu Ser  
 130 135 140  
 Leu Thr Lys Leu Glu Arg Tyr Arg Tyr Glu Ile Leu Leu Glu Ala Val  
 145 150 155 160  
 Ala Ala Asp Arg Leu Pro Leu Ile Glu Leu Thr Lys Asp Glu Phe Lys  
 165 170 175  
 His Ala Thr Glu Glu Asp Lys Thr Arg Ile Arg Tyr Leu Ile Thr Glu  
 180 185 190  
 Gln Phe Glu Ala Trp Gln Lys Gln Lys Tyr Gln Lys Glu Leu Ala Leu  
 195 200 205  
 Gln Arg Arg Glu Ala Glu Lys Gln Thr Val Leu Ala Asn Ile Arg Lys  
 210 215 220  
 Tyr Glu Gly Ile Ser Arg Val Glu Asn Glu Arg Leu Lys Asp Leu Lys  
 225 230 235 240  
 Lys Leu Phe Asn Ser Lys Ser Thr Ser Lys His Asp Val Leu Thr Gln  
 245 250 255  
 Glu Asn Arg His Ile Glu Ala Val Asn Glu Leu Ala Val Tyr Lys Ser  
 260 265 270  
 Arg Leu Asn Glu Val Glu Ser Asp Leu Arg Gln Ala Lys Glu Glu Ile  
 275 280 285  
 His Leu Ile Thr Gln Leu Phe Arg Ala Asp Ile Leu Glu Lys Leu Lys  
 290 295 300  
 Gln Asn Val Glu Ala Glu Lys Gln Leu Ser Leu Glu Leu Glu Lys Asn  
 305 310 315 320  
 Glu Gln Arg Gln Ile Ala Ser Val Ile Arg Ala Pro Val Ser Gly Thr  
 325 330 335  
 Val Gln Gln Leu Lys Thr His Thr Val Gly Gly Val Val Thr Thr Ala  
 340 345 350  
 Glu Thr Leu Met Val Ile Ala Pro Glu Asp Asp Val Leu Glu Val Thr  
 355 360 365

Ala Leu Ile Gln Asn Lys Asp Ile Gly Phe Ile Glu Val Gly Gln Asp  
 370 375 380

Ala Val Ile Lys Val Glu Thr Phe Pro Tyr Thr Arg Tyr Gly Tyr Leu  
 385 390 395 400

Met Gly Lys Val Lys Asn Ile Thr Leu Glu Ala Ile Glu His Pro Gln  
 405 410 415

Leu Gly Leu Val Phe Asn Ser Ile Ile Ser Ile Asp Arg Lys Thr Leu  
 420 425 430

Ser Gly Lys Asp Gly Lys Glu Ile Glu Leu Gly Ser Gly Met Ser Val  
 435 440 445

Thr Ala Glu Ile Lys Thr Gly Glu Arg Ser Val Ile Ser Tyr Leu Leu  
 450 455 460

Ser Pro Leu Glu Glu Ser Val Ser Glu Ser Leu Arg Glu Arg  
 465 470 475

<210> 40  
 <211> 478  
 <212> PRT  
 <213> Escherichia coli

<400> 40  
 Met Lys Thr Trp Leu Met Gly Phe Ser Glu Phe Leu Leu Arg Tyr Lys  
 1 5 10 15

Leu Val Trp Ser Glu Thr Trp Lys Ile Arg Lys Gln Leu Asp Thr Pro  
 20 25 30

Val Arg Glu Lys Asp Glu Asn Glu Phe Leu Pro Ala His Leu Glu Leu  
 35 40 45

Ile Glu Thr Pro Val Ser Arg Arg Pro Arg Leu Val Ala Tyr Phe Ile  
 50 55 60

Met Gly Phe Leu Val Ile Ala Phe Ile Leu Ser Val Leu Gly Gln Val  
 65 70 75 80

Glu Ile Val Ala Thr Ala Asn Gly Lys Leu Thr Leu Ser Gly Arg Ser  
 85 90 95

Lys Glu Ile Lys Pro Ile Glu Asn Ser Ile Val Lys Glu Ile Ile Val  
 100 105 110

Lys Glu Gly Glu Ser Val Arg Lys Gly Asp Val Leu Leu Lys Leu Thr  
 115 120 125

Ala Leu Gly Ala Glu Ala Asp Thr Leu Lys Thr Gln Ser Ser Leu Leu  
 130 135 140

Gln Ala Arg Leu Glu Gln Ile Arg Tyr Gln Ile Leu Ser Arg Ser Ile  
 145 150 155 160

Glu Leu Asn Lys Leu Pro Glu Leu Lys Leu Pro Asp Glu Pro Tyr Phe  
 165 170 175  
 Gln Asn Val Ser Glu Glu Glu Val Leu Arg Leu Thr Ser Leu Ile Lys  
 180 185 190  
 Glu Gln Phe Ser Thr Trp Gln Asn Gln Lys Tyr Gln Lys Glu Leu Asn  
 195 200 205  
 Leu Asp Lys Lys Arg Ala Glu Arg Leu Thr Ile Leu Ala Arg Ile Asn  
 210 215 220  
 Arg Tyr Glu Asn Val Ser Arg Val Glu Lys Ser Arg Leu Asp Asp Phe  
 225 230 235 240  
 Arg Ser Leu Leu His Lys Gln Ala Ile Ala Lys His Ala Val Leu Glu  
 245 250 255  
 Gln Glu Asn Lys Tyr Val Glu Ala Ala Asn Glu Leu Arg Val Tyr Lys  
 260 265 270  
 Ser Gln Leu Glu Gln Ile Glu Ser Glu Ile Leu Ser Ala Lys Glu Glu  
 275 280 285  
 Tyr Gln Leu Val Thr Gln Leu Phe Lys Asn Glu Ile Leu Asp Lys Leu  
 290 295 300  
 Arg Gln Thr Thr Asp Ser Ile Glu Leu Leu Thr Leu Glu Leu Glu Lys  
 305 310 315 320  
 Asn Glu Glu Arg Gln Gln Ala Ser Val Ile Arg Ala Pro Val Ser Gly  
 325 330 335  
 Lys Val Gln Gln Leu Lys Val His Thr Glu Gly Gly Val Val Thr Thr  
 340 345 350  
 Ala Glu Thr Leu Met Val Ile Val Pro Glu Asp Asp Thr Leu Glu Val  
 355 360 365  
 Thr Ala Leu Val Gln Asn Lys Asp Ile Gly Phe Ile Asn Val Gly Gln  
 370 375 380  
 Asn Ala Ile Ile Lys Val Glu Ala Phe Pro Tyr Thr Arg Tyr Gly Tyr  
 385 390 395 400  
 Leu Val Gly Lys Val Lys Asn Ile Asn Leu Asp Ala Ile Glu Asp Gln  
 405 410 415  
 Lys Leu Gly Leu Val Phe Asn Val Ile Val Ser Val Glu Glu Asn Asp  
 420 425 430  
 Leu Ser Thr Gly Asn Lys His Ile Pro Leu Ser Ser Gly Met Ala Val  
 435 440 445  
 Thr Ala Glu Ile Lys Thr Gly Met Arg Ser Val Ile Ser Tyr Leu Leu  
 450 455 460

Ser Pro Leu Glu Glu Ser Val Thr Glu Ser Leu His Glu Arg  
465 470 475

<210> 41  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<220>  
<221> modified\_base  
<222> (14)  
<223> a, t, c, g, other or unknown

<400> 41  
tagtaaattta aatnactwaa cact